

(1) GENERAL INFORMATION

(ii) TITLE OF THE INVENTION: NEW GLUTATHIONE-S-TRANSFERASE

(iv) CORRESPONDENCE ADDRESS:

(v) COMPUTER READABLE FORM:

(vi) CURRENT APPLICATION DATA:

(vii) PRIOR APPLICATION DATA:

(viii) ATTORNEY/AGENT INFORMATION:

(ix) TELECOMMUNICATION INFORMATION:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(vii) IMMEDIATE SOURCE:

53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Pro Leu Pro Arg Thr Val Glu Leu Phe Tyr Asp Val Leu Ser
 1 5 10 15
 Pro Tyr Ser Trp Leu Gly Phe Glu Ile Leu Cys Arg Tyr Gln Asn Ile
 20 25 30
 Trp Asn Ile Asn Leu Gln Leu Arg Pro Ser Leu Ile Thr Gly Ile Met
 35 40 45
 Lys Asp Ser Gly Asn Lys Pro Gly Leu Leu Pro Arg Lys Gly Leu
 50 55 60
 Tyr Met Ala Asn Asp Leu Lys Leu Leu Arg His His Leu Gln Ile Pro
 65 70 75 80
 Ile His Phe Pro Lys Asp Phe Leu Ser Val Met Leu Glu Lys Gly Ser
 85 90 95
 Leu Ser Ala Met Arg Phe Leu Thr Ala Val Asn Leu Glu His Pro Glu
 100 105 110
 Met Leu Glu Lys Ala Ser Arg Glu Leu Trp Met Arg Val Trp Ser Arg
 115 120 125
 Asn Glu Asp Ile Thr Glu Pro Gln Ser Ile Leu Ala Ala Ala Glu Lys
 130 135 140
 Ala Gly Met Ser Ala Glu Gln Ala Gln Gly Leu Leu Glu Lys Ile Ala
 145 150 155 160
 Thr Pro Lys Val Lys Asn Gln Leu Lys Glu Thr Thr Glu Ala Ala Cys
 165 170 175
 Arg Tyr Gly Ala Phe Gly Leu Pro Ile Thr Val Ala His Val Asp Gly
 180 185 190
 Gln Thr His Met Leu Phe Gly Ser Asp Arg Met Glu Leu Leu Ala His
 195 200 205
 Leu Leu Gly Glu Lys Trp Met Gly Pro Ile Pro Pro Ala Val Asn Ala
 210 215 220
 Arg Leu
 225

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT04
- (B) CLONE: 1554593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGCAGCCTC	TGCCGGGTTC	CGGGAAAAGG	AGCTCCTGCT	GCCACTGCTC	TTCCGGAGCC	60
TGCAGCATGG	GGCCCCTGCC	GCGCACCGTG	GAGCTCTTCT	ATGACGTGCT	GTCCCCCTAC	120
TCCTGGCTGG	GCTTCGAGAT	CCTGTGCCGG	TATCAGAATA	TCTGGAACAT	CAACCTGCAG	180
TTGCGGCCCA	GCCTCATAAC	AGGGATCATG	AAAGACAGTG	GAAACAAGCC	TCCAGGTCTG	240
CTTCCCCGCA	AAGGACTATA	CATGGCAAAT	GACTTAAAGC	TCCTGAGACA	CCATCTCCAG	300
ATTCCCATCC	ACTTCCCCAA	GGATTTCTTG	TCTGTGATGC	TTGAAAAAGG	AAGTTTGTCT	360
GCCATGCGTT	TCCTCACCGC	CGTGAACCTG	GAGCATCCAG	AGATGCTGGA	GAAAGCGTCC	420
CGGGAGCTGT	GGATGCGCGT	CTGGTCAAGG	AATGAAGACA	TCACCGAGCC	GCAGAGCATC	480
CTGGCGGCTG	CAGAGAAGGC	TGGTATGTCT	GCAGAACAAG	CCCAGGGACT	TCTGGAAAAG	540
ATCGCAACGC	CAAAGGTGAA	GAACCAGCTC	AAGGAGACCA	CTGAGGCAGC	CTGCAGATAC	600
GGAGCCTTTG	GGCTGCCCAT	CACCGTGGCC	CATGTGGATG	GCCAAACCCA	CATGTTATTT	660
GGCTCTGACC	GGATGGAGCT	GCTGGCGCAC	CTGCTGGGAG	AGAAGTGGAT	GGGCCCTATA	720
CCTCCAGCCG	TGAATGCCAG	ACTTTAAGAT	TGCCCCGAGG	AAGCAAATC	TTCGTATAAA	780
AAAAGCAGGC	CATCTGCTTA	ACCCTTGGCT	CCACCATAAG	GCACTGGGAC	TCGGATTTC	840

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CTATCTGATA GAGGTATTTT CTGTGGCCCT GGGAGCTGTC TGTCTTTCCC CTACCCCCAA 900
GGATGCCAGG AAGACGTCCA CCATTAGCCA TGTGGCAACC TTTACTTCTA TGCCTCACAA 960
GTGCCTTTCA GAGAGCCCCA ATTCTGCTTT CCCACAAAAT AAACCTAATG CCATCAGGCA 1020
AAACAAAAAA AAAAA 1035

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: ?

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Gly Pro Ala Pro Arg Val Leu Glu Leu Phe Tyr Asp Val Leu Ser
 1          5          10          15
Pro Tyr Ser Trp Leu Gly Phe Glu Val Leu Cys Arg Tyr Gln His Leu
 20          25          30
Trp Asn Ile Lys Leu Lys Leu Arg Pro Ala Leu Leu Ala Gly Ile Met
 35          40          45
Lys Asp Ser Gly Asn Gln Pro Pro Ala Met Val Pro His Lys Gly Gln
 50          55          60
Tyr Ile Leu Lys Glu Ile Pro Leu Leu Lys Gln Leu Phe Gln Val Pro
 65          70          75          80
Met Ser Val Pro Lys Asp Phe Phe Gly Glu His Val Lys Lys Gly Thr
 85          90          95
Val Asn Ala Met Arg Phe Leu Thr Ala Val Ser Met Glu Gln Pro Glu
100          105          110
Met Leu Glu Lys Val Ser Arg Glu Leu Trp Met Arg Ile Trp Ser Arg
115          120          125
Asp Glu Asp Ile Thr Glu Ser Gln Asn Ile Leu Ser Ala Ala Glu Lys
130          135          140
Ala Gly Met Ala Thr Ala Gln Ala Gln His Leu Leu Asn Lys Ile Ser
145          150          155          160
Thr Glu Leu Val Lys Ser Lys Leu Arg Glu Thr Thr Gly Ala Ala Cys
165          170          175
Lys Tyr Gly Ala Phe Gly Leu Pro Thr Thr Val Ala His Val Asp Gly
180          185          190
Lys Thr Tyr Met Leu Phe Gly Ser Asp Arg Met Glu Leu Leu Ala Tyr
195          200          205
Leu Leu Gly Glu Lys Trp Met Gly Pro Val Pro Pro Thr Leu Asn Ala
210          215          220
Arg Leu
225

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